

RESULT	2	CHKESTFLUA				1383 bp	mRNA	VRT	12-DEC-1996
LOCUS									
DEFINITION	Chicken mRNA for unknown protein, complete cds.								
ACCESSION	D26311								
NID	g517092								
KEYWORDS	.								
SOURCE	Gallus gallus lens fibers cDNA to mRNA, clone CLFEST4.								
ORGANISM	Gallus gallus								
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;								
	Vertebrata; Archosauria; Aves; Neognathae; Galliformes;								
	Phasianidae; Phasianinae; Gallus.								
REFERENCE	1 (sites)								
AUTHORS	Sawada,K., Agata,K. and Eguchi,G.								
TITLE	Characterization of terminally differentiated cell state by categorizing cDNA clones derived from chicken lens fibers								
JOURNAL	Int. J. Dev. Biol. 40 (3), 531-535 (1996)								
MEDLINE	96437509								
REFERENCE	2 (bases 1 to 1383)								
AUTHORS	Sawada,K., Agata,K. and Eguchi,G.								
TITLE	Analysis of the cDNA library of chicken lens fibers: identification of a cDNA coding a novel leucine zipper protein which has constructive similarities with the CREB family								
JOURNAL	Unpublished (1994)								
REFERENCE	3 (bases 1 to 1383)								
AUTHORS	Sawada,K.								
TITLE	Direct Submission								
JOURNAL	Submitted (25-DEC-1993) to the DDBJ/EMBL/GenBank databases.								
	Kaichiro Sawada, Biohistory Research Hall; 1-1 Murasaki-cho, Takatsuki, Osaka 569-11, Japan								
	(E-mail:Kaichiro.Sawada@ims.brh.co.jp, Tel:0726-81-9754, Fax:0726-81-9757)								
FEATURES	Location/Qualifiers								
source	1. .1383								
	/organism="Gallus gallus"								
	/db_xref="taxon:9031"								
	/clone="CLFEST4"								
	/tissue_type="lens fibers"								
CDS	36. .1088								
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	/db_xref="PID:g517093"								
	/translation="MRRGEGPAPRRRWLLLLAVLAALCCAAAGSGGRRRAASLGEMLR								
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	THQEIDKVTDNRTGSTIFSETIITSIKGGENKRNHECIIDEDCETGKYQFSTFEYKC								
	QPCKTQHTHCSRDEVECCGDLQCVWGECRKATSRGENGTICENQHD CNP GTCCAFQKEL								
	LFPVCTPLPEEGEPCHDPSNRLLNLITWELEPDGVLERPCASGLICQPQSSHSTTSV								
	CELSSNETRKNEKEDPLNMDEMPFISLIPRILSDYEESSVIQEV RKELESLEDQAGV								
	KSEHDPADHLFLGDEI"								
polyA_site	1383								
BASE COUNT	414 a	306 c	352 g	311 t					
ORIGIN									

Query Match 28.0%; Score 294; DB 17; Length 1383;
Best Local Similarity 71.0%; Pred. No. 1.67e-195;
Matches 497; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

Db	143	GGCCAGCCTGGGCGAGATGCTGCGGAGGTTGAGGCGCTGATGGAGGACACGCGACACAA	202
Qy	132	GGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTATGGAGGACACGCGACACAA	191
Db	203	GCTGCGCAACGCGGTGCAGGAGATGGAAGCTGAAGAAGAAGGGGCAAAAAAAGTGTCTGAGA	262
Qy	192	ATTGCGCAGCGCGTGAAGAGATGGAGGCAGAAGAAGCTGCTGCTAAAGCATCATCAGA	251
Db	263	AGTAAACTTTGAAAAGTTACCTCCCACCTACCATAATGAGTCCAACACAGAAACCAGAAT	322
Qy	252	AGTGAACCTGGCAAAGTTACCTCCCAGCTATCACAAATGAGACCAACACAGACACGAACGT	311
Db	323	TGGTAATAAAAGTGTTCAGACTCATCAAGAAATTGATAAGGTTACAGATAACAGAACTGG	382
Qy	312	TGGAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACAGACTGG	371

Untitled

Db	383	ATCAACAATTTTTCCGAGACAATTATTACATCTATAAAGGGTGGAGAAAACAAAAGAAA	442
Qy	372	ACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAG	431
Db	443	TCATGAGTGTATCATTGATGAAGACTGTGAAACAGGAAAGTATTGCCAGTTCTCCACCTT	502
Qy	432	CCACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTT	491
Db	503	TGAATACAAGTGTACGCCCTGTAAAACCCAGCATACACACTGCTCACGAGATGTTGAATG	562
Qy	492	CCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTG	551
Db	563	CTGCGGAGACCAGCTTTGTGTTTGGGGTGAGTGCAGGAAAGCCACTTCAAGAGGAGAAAA	622
Qy	552	CTGTGGAGACCAGCTGTGTGCTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAA	611
Db	623	TGGTACCATTGTGTGAGAACCAACATGACTGCAACCCAGGAACGTGCTGTGCTTTTCAGAA	682
Qy	612	TGGGACCATCTGTGACAACAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAG	671
Db	683	AGAACTGCTGTTTCCTGTGTGCACTCCGTTACCCGAAGAAGGTGAACCTTGCCATGATCC	742
Qy	672	AGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCC	731
Db	743	TTCAAACAGACTTCTCAACCTGATCACCTGGGAACCTGGAACCTGATGGAGTACTAGAGCG	802
Qy	732	CGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATGGAGCCTTGACCG	791
Db	803	CTGCCCATGTGCAAGTGGCTTGATCTGCCAACCTCAGAGC	842
Qy	792	ATGGCCCTGTGCCAGTGGCCCTCCTCTGCCAGCCCCACAG	831